SEQUENCE LISTING

<110> Zonana et al.

<120> Hypohydrotic ectodermal dysplasia genes and proteins

<130> 55924

<140> 09/729,658
<141> 2000-12-04

<150> 09/342,681
<151> 1999-06-29

<150> 60/092,279
<151> 1998-07-09

<150> 60/112,366
<151> 1998-12-15

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<170> PatentIn Ver. 2.1

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gaacggctga ggcagacgca gcggctcccg ggcctcaaga gagtgggtgt ctccggaggc 240

c atg ggc tac ccg gag gtg gag cgc agg gaa ctc ctg cct gca gca gcg 289
  Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala
  1   5   10   15

ccg cgg gag cga ggg agc cag ggc tgc ggg tgt ggc ggg gcc cct gcc   337
Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
            20   25   30

cgg gcg ggc gaa ggg aac agc tgc ctg ctc ttc ctg ggt ttc ttt ggc   385
Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
        35   40   45

ctc tcg ctg gcc ctc cac ctg ctg acg ttg tgc tgc tac cta gag ttg   433
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu

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cgc tcg gag ttg cgg cgg gaa cgt gga gcc gag tcc cgc ctt ggc ggc     481
Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
65                  70                      75                  80

tcg ggc acc cct ggc acc tct ggc acc cta agc agc ctc ggt ggc ctc     529
Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
                    85                  90                  95

gac cct gac agc ccc atc acc agt cac ctt ggg cag ccg tca cct aag     577
Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
                100                 105                 110

cag cag cca ttg gaa ccg gga gaa gcc gca ctc cac tct gac tcc cag     625
Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
                115                 120                 125

gac ggg cac cag atg gcc cta ttg aat ttc ttc ttc cct gat gaa aag     673
Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
                130                 135                 140

cca tac tct gaa gaa gaa agt agg cgt gtt cgc cgc aat aaa aga agc     721
Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145                 150                 155                 160

aaa agc aat gaa gga gca gat ggc cca gtt aaa aac aag aaa aag gga     769
Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
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aag aaa gca gga cct cct gga ccc aat ggc cct cca gga ccc cca gga     817
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
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cct cca gga ccc cag gga ccc cca gga att cca ggg att cct gga att     865
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
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cca gga aca act gtt atg gga cca cct ggt cct cca ggt cct cct ggt     913
Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
210                 215                 220

cct caa gga ccc cct ggc ctc cag gga cct tct ggt gct gct gat aaa     961
Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225                 230                 235                 240

gct gga act cga gaa aac cag cca gct gtg gtg cat cta cag ggc caa     1009
Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
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ggg tca gca att caa gtc aag aat gat ctt tca ggt gga gtg ctc aat     1057
Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
                260                 265                 270

gac tgg tct cgc atc act atg aac ccc aag gtg ttt aag cta cat ccc     1105
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
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2

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agt cag gta gaa gta tac tac atc aac ttc act gac ttt gcc agc tat   1201
Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
305             310             315             320

gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc aca cgc agc atc   1249
Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
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gag acg ggc aag acc aac tac aac act tgc tat acc gca ggc gtc tgc   1297
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        340             345             350

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Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
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atc tcc atc aac atg agc aag cac acc acg ttc ttt ggg gcc atc agg   1393
Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
        370             375             380

ctg ggt gaa gcc cct gca tcc tag attcccccat tttgcctctg tccgtgcccc   1447
Leu Gly Glu Ala Pro Ala Ser
385             390

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<213> Homo sapiens

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            35                  40                  45
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
        50                  55                  60
Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
65                  70                  75                  80
Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
                85                  90                  95
Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
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              115                    120                    125
    Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
        130                    135                    140
    Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
    145                    150                    155                    160
    Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
                   165                    170                    175
    Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
                   180                    185                    190
    Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
               195                    200                    205
    Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
        210                    215                    220
    Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
    225                    230                    235                    240
    Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
                   245                    250                    255
    Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
                   260                    265                    270
    Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
               275                    280                    285
    Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
        290                    295                    300
    Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
    305                    310                    315                    320
    Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
                   325                    330                    335
    Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
               340                    345                    350
    Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
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tagtggttgt ctctggaggc c atg ggc tac cca gag gta gag cgc agg gaa     171
                        Met Gly Tyr Pro Glu Val Glu Arg Arg Glu
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4

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                15                  20                  25

tgt cgc ggg gcc cct gct cgg gcg ggc gaa ggg aac agc tgc cgg ctc    267
Cys Arg Gly Ala Pro Ala Arg Ala Gly Glu Gly Asn Ser Cys Arg Leu
                30                  35                  40

ttc ctg ggt ttc ttt ggc ctc tcg ctg gcc ctc cac ctg ctg acg ctg    315
Phe Leu Gly Phe Phe Gly Leu Ser Leu Ala Leu His Leu Leu Thr Leu
                45                  50                  55

tgc tgc tac cta gag ttg cgg tcc gaa ttg cgg cgg gaa cgg gga acc    363
Cys Cys Tyr Leu Glu Leu Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr
        60                  65                  70

gag tcc cgc ctc ggt ggc ccg ggt gct cct ggc acc tct ggc acc cta    411
Glu Ser Arg Leu Gly Gly Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu
75                  80                  85                  90

agc agc cct ggg agc ctc gac ccg gtg ggt ccc atc acc cgc cac ctg    459
Ser Ser Pro Gly Ser Leu Asp Pro Val Gly Pro Ile Thr Arg His Leu
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ggg cag ccg tcc ttt caa cag cag cct ttg gaa ccg gga gaa gat cca    507
Gly Gln Pro Ser Phe Gln Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro
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ctc ccc cct gag tcc cag gac cgg cac cag atg gcc ctc ctg aat ttc    555
Leu Pro Pro Glu Ser Gln Asp Arg His Gln Met Ala Leu Leu Asn Phe
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ttc ttt cct gat gaa aag gca tat tct gaa gag gaa agt agg cgt gtt    603
Phe Phe Pro Asp Glu Lys Ala Tyr Ser Glu Glu Glu Ser Arg Arg Val
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cgc cgc aat aag aga agc aaa agt ggt gaa gga gca gat ggt cct gtt    651
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155                 160                 165                 170

aaa aac aag aaa aag gga aag aag gca ggg cca cct ggg ccc aac ggc    699
Lys Asn Lys Lys Lys Gly Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly
                175                 180                 185

ccc cca gga cct cca gga cct ccg gga ccc cag gga cct cca ggg att    747
Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile
                190                 195                 200

cca gga att cct ggg att cca gga aca act gtt atg gga cca cct ggc    795
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                205                 210                 215

cca cct ggc cct cct ggt cct caa gga ccc cct ggc ctc caa gga cct    843
Pro Pro Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro
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Ser Gly Ala Ala Asp Lys Thr Gly Thr Arg Glu Asn Gln Pro Ala Val
235              240              245              250

gtg cat ctg cag ggc caa ggg tca gca att caa gtc aaa aat gat ctt    939
Val His Leu Gln Gly Gln Gly Ser Ala Ile Gln Val Lys Asn Asp Leu
                 255              260              265

tca ggt gga gtg ctc aat gac tgg tct cgc atc act atg aac cct aag    987
Ser Gly Gly Val Leu Asn Asp Trp Ser Arg Ile Thr Met Asn Pro Lys
                 270              275              280

gtg ttt aaa cta cat ccc cgc agc ggg gag ctg gag gtc tac tac atc   1035
Val Phe Lys Leu His Pro Arg Ser Gly Glu Leu Glu Val Tyr Tyr Ile
             285              290              295

aac ttc act gac ttt gcc agc tac gag gtg gtg gtg gat gag aag ccc   1083
Asn Phe Thr Asp Phe Ala Ser Tyr Glu Val Val Val Asp Glu Lys Pro
             300              305              310

ttc ctg cag tgc acc cgc agc att gag aca ggg aag acc aac tac aac   1131
Phe Leu Gln Cys Thr Arg Ser Ile Glu Thr Gly Lys Thr Asn Tyr Asn
315              320              325              330

act tgc tat act gca ggc gtg tgc ctc ctc aag gcc agg cag aaa atc   1179
Thr Cys Tyr Thr Ala Gly Val Cys Leu Leu Lys Ala Arg Gln Lys Ile
                 335              340              345

gcc gtg aag atg gtg cac gct gac atc tct atc aat atg agc aag cac   1227
Ala Val Lys Met Val His Ala Asp Ile Ser Ile Asn Met Ser Lys His
                 350              355              360

acc acc ttc ttc ggg gcc atc agg ctg ggc gaa gcc cct gca tcc tag   1275
Thr Thr Phe Phe Gly Ala Ile Arg Leu Gly Glu Ala Pro Ala Ser
                 365              370              375

attctcccat tccatcctgg cccatgcccc tgccccaggt ttgggagcca ggactcccag 1335

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gaaagacctt gagttgccag gacagttgac ggagccccag ggttgtcaag aagcagaacc 1515

ttcttaggct ccctgctgac tggcttatgg tgactcctca acccttaggt ccctcatcag 1575

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<213> Mus musculus

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Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
    50                  55                  60
Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr Glu Ser Arg Leu Gly Gly
65              70                  75                  80
Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu Ser Ser Pro Gly Ser Leu
                85                  90                  95
Asp Pro Val Gly Pro Ile Thr Arg His Leu Gly Gln Pro Ser Phe Gln
            100                 105                 110
Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro Leu Pro Pro Glu Ser Gln
        115                 120                 125
Asp Arg His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
    130                 135                 140
Ala Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145                 150                 155                 160
Lys Ser Gly Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
                165                 170                 175
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
            180                 185                 190
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
        195                 200                 205
Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
    210                 215                 220
Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225                 230                 235                 240
Thr Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
                245                 250                 255
Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
            260                 265                 270
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
        275                 280                 285
Arg Ser Gly Glu Leu Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala
    290                 295                 300
Ser Tyr Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg
305                 310                 315                 320
Ser Ile Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly
                325                 330                 335
Val Cys Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His
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<213> Homo sapiens

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<223> n represents a, c, t, or g

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gtatcctttt aagaactacc ttcttggtag ggcatggtgg ctcacgcctg taatcctagc 360
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aacatggtga aaccctgtct ctactaaaaa tacaaaaaaa attagccggg cctagtccca 480
gctgcttggg agactaaggc aggagaatcg cttgaaactg ggaggtagag gttgcagtga 540
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caaaaacaaa caaaaaaaaa cactaccttt 630
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<211> 549
<212> DNA
<213> Homo sapiens

<400> 6

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tccttgccaa aagcctgacc cttggctgtg agactccctc aaatttgcag tgtcttgggg 180
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tatctatttt attttttctta taggcccagt taaaaacaag aaaaagggta agttcctgac 300
tttataaaat tgctgtcttg tcatatattt tctaaagtta gaagaaaaaa acaagagtgc 360
gatttttgta ttatattctt tcagcattgt ctgtctgtta ttttattcaa tcatatgtta 420
tcttcttgag tattgtagtt tctgaagaac aagaaatcat tcttcagtga tgattcacct 480
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<210> 7
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<212> DNA
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<400> 7

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gtggcaagcg cctgtaatcc cagttaatcc agaggctgag gcaggagaat tgcttgaacc 180
cgggaggtgg aggttgcagt gagccgagat tgtgccactg aactccagcc tgggcaacag 240
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<212> DNA
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<212> DNA
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tggattacaa tagaagacta gaaaccagga tggaaacatg ggactggtgg ctgagcaagc 540
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cccaaagagg agcttctccc ctgcctcctc cccagcctcc aaataatcac ccagcctagt 720
tcctcccagg ccgctgaggt accgttggca tacnaagtca ttctttgctc catcatgccc 780
tctactggct gtcctgagca attgctggca tcaagaccag ttgctacacc caaattgctt 840

9

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tagaatcact gatgacggag ctgaaaggga cttgagacat catctagccc aggcattctc 900
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<212> DNA
<213> Homo sapiens
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aagaaaggaa ggataaagac agacaggcag agcccaggag ccctgaagca ggcctggcag 180
ctgctttaca aacagaacag cttctctgct ttcaaatgct cttcttaaag tttggccttc 240
taggctaccc tggttgcact gggatagggg tggggggttgt gaactccttg gtatttattt 300
tctgttgcct cgattattct gacatgtact gagtgactgc cttctctcat actgagatct 360
ttcaggtgga gtgctcaatg actggtctcg catcactatg aaccccaagg tgtttaagct 420
acatccccgc agcggggagc tggaggtact ggtggacggc acctacttca tctatagtca 480
ggtagaagtg agtacggtct taggcctaac tcttcttata tccagaatgc agatccggtg 540
caggccacat aggggcactg tggagccagc caagaccatc caatggctaa cttcctgctt 600
tgggtgaggg ggtgggggga ccgcactggg agggagttga aaggaggaaa gagagagggg 660
gccagcttct tttgttttgt tttgttttgt ttttccctac ccaaatatta ttgaaaaact 720
gtgaaaaaga ccctcccaca ccctgccatc tgattccctc ctgcagggcc tcaggcccct 780
gtttaccctc tgagctgttt ggctgcactg ccaaacttga acttggtctc a          831
```

```
<210> 11
<211> 743
<212> DNA
<213> Homo sapiens
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<220>
<221> misc_feature
<222> (302)
<223> n represents a, c, t, or g
```

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<400> 11
gcttcatgtc agggctgggg caggggtggg cggggaaaca ggggcacggt gaagctgcaa 60
atagggcatg gttcttagcc ttacagagtt tgcgacaagt gtgctgttgt aagaaaagtt 120
tgctcagcca gctgagcccc atggactagg ggaagaacaa tgcctgtcac ctgtcctttc 180
ctgttggcca gctagcacgc cttcacatgg cactgcccca tccatggggt atactaacag 240
ctcatctgag aagattctgt caattcacca cagggagggc cccccaccct ctctttcctc 300
tnttccccaa tcccttcttg ttgcctctca tcaggtatac tacatcaact tcactgactt 360
tgccagctat gaggtggtgg tggatgagaa gcccttcctg cagtgcacac gcagcatcga 420
gacgggcaag accaactaca acacttgcta taccgcaggc gtctgcctcc tcaaggcccg 480
gcagaagatc gccgtcaaga tggtgcacgc tgacatctcc atcaacatga gcaagcacac 540
cacgttcttt ggggccatca ggctgggtga agcccctgca tcctagattc ccccattttg 600
cctctgtccg tgccccttcc ctgggtttgg gagccaggac tcccaaaacc tctaagtgct 660
gctgtggagt gaggtgtatt ggtgttgcag ccgcagagaa atgccccatt gttatttatt 720
ccccagtgac tccagggtga caa                                         743
```

```
<210> 12
<211> 3720
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10

<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (260)..(1606)

<220>
<221> misc_feature
<222> (2961)..(3673)
<223> n represents a, c, t, or g

<400> 12

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cagtccagac cgggaacagt caagagcgag ttcccgggag cccttcaaaa tagaaagtta 60

gttgcgctgg cagcagaggt gtgcctggcc gctgtcaccc ggctggcccc aggattgtgg 120

agctctgctt ttgagaggac accgacggac gcctgtgaag cctgccccc atcccttacc 180

tgctcgcctt ctccgtagac ccatcttctg ctgggaaaag ctaacctcat tcgggtacca 240

ggtgtacttc caagagatc atg gcc cac gtc ggg gac tgc aaa tgg atg tcc   292
                        Met Ala His Val Gly Asp Cys Lys Trp Met Ser
                        1                5                        10

tgg ctc cca gtg ctg gtg gtg tct ctg atg tgc tca gcc aag gcg gag   340
Trp Leu Pro Val Leu Val Val Ser Leu Met Cys Ser Ala Lys Ala Glu
              15               20                   25

gac tcc aac tgt ggt gag aac gaa tac cac aac cag act acc ggg ctg   388
Asp Ser Asn Cys Gly Glu Asn Glu Tyr His Asn Gln Thr Thr Gly Leu
          30               35                   40

tgc cag cag tgt cct cca tgc aga cca ggg gag gag ccc tac atg tcc   436
Cys Gln Gln Cys Pro Pro Cys Arg Pro Gly Glu Glu Pro Tyr Met Ser
          45               50                   55

tgt gga tac ggc act aaa gac gac gac tat ggc tgt gtg ccc tgc cct   484
Cys Gly Tyr Gly Thr Lys Asp Asp Asp Tyr Gly Cys Val Pro Cys Pro
60                   65               70                   75

gca gag aag ttc tcc aaa gga ggt tat cag ata tgc agg cgc cac aaa   532
Ala Glu Lys Phe Ser Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys
                  80               85                   90

gac tgt gag ggc ttc ttc cgg gcc act gtg ctg aca cca gga gac atg   580
Asp Cys Glu Gly Phe Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met
              95                   100                  105

gaa aac gac gct gag tgt ggc cca tgt ctc cct ggc tac tac atg ctg   628
Glu Asn Asp Ala Glu Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu
              110                  115                  120

gaa aac aga ccc agg aac atc tat ggc atg gtc tgc tac tcc tgt ctc   676
Glu Asn Arg Pro Arg Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu
              125                  130                  135
```

11

```
ttg gca cct ccc aac acc aag gaa tgt gtg gga gcc act tct ggg gtt    724
Leu Ala Pro Pro Asn Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Val
140                 145                 150                 155

tca gca cac tca tcc agc act tcc ggt ggc agc acc ttg tct ccc ttc    772
Ser Ala His Ser Ser Ser Thr Ser Gly Gly Ser Thr Leu Ser Pro Phe
                160                 165                 170

cag cat gct cac aaa gag ctc tca ggc caa gga cac ctg gcc acc gcc    820
Gln His Ala His Lys Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala
                175                 180                 185

ctg att att gcc atg tct acg atc ttc atc atg gcc att gcc atc gtc    868
Leu Ile Ile Ala Met Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val
            190                 195                 200

ctc atc atc atg ttc tac atc atg aag act aag ccg tca gct cca gcc    916
Leu Ile Ile Met Phe Tyr Ile Met Lys Thr Lys Pro Ser Ala Pro Ala
            205                 210                 215

tgc tgt agc agt ccc cca gga aag agc gca gaa gcc cca gct aac aca    964
Cys Cys Ser Ser Pro Pro Gly Lys Ser Ala Glu Ala Pro Ala Asn Thr
220                 225                 230                 235

cac gag gag aaa aaa gag gcc cca gac agt gtg gtg acg ttc cct gag   1012
His Glu Glu Lys Lys Glu Ala Pro Asp Ser Val Val Thr Phe Pro Glu
                240                 245                 250

aat ggt gag ttc cag aag ctg aca gca aca ccc aca aag acc ccc aaa   1060
Asn Gly Glu Phe Gln Lys Leu Thr Ala Thr Pro Thr Lys Thr Pro Lys
                255                 260                 265

agt gag aat gat gcc tcc tct gag aac gag cag ttg cta agt cgc agt   1108
Ser Glu Asn Asp Ala Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser
                270                 275                 280

gtg gac agt gat gaa gag cca gcc ccg gac aag cag ggg tcc cca gag   1156
Val Asp Ser Asp Glu Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu
            285                 290                 295

cta tgt ctg ctg tcg cta gtt cac ctg gcc agg gag aag tct gtg acc   1204
Leu Cys Leu Leu Ser Leu Val His Leu Ala Arg Glu Lys Ser Val Thr
300                 305                 310                 315

agt aac aag tct gct ggg atc cag agc cgg agg aaa aag ata ctg gat   1252
Ser Asn Lys Ser Ala Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp
                320                 325                 330

gtg tat gcc aac gtg tgt ggt gtt gtt gaa ggt ctc agc ccc acc gag   1300
Val Tyr Ala Asn Val Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu
                335                 340                 345

ttg ccg ttt gac tgc ctt gag aag aca agc cga atg ctc agc tct aca   1348
Leu Pro Phe Asp Cys Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr
                350                 355                 360
```

12

```
tac aac tct gag aag gcg gtc gtg aaa aca tgg cgc cac ctt gcc gag    1396
Tyr Asn Ser Glu Lys Ala Val Val Lys Thr Trp Arg His Leu Ala Glu
    365                 370                 375

agc ttt gga ctg aag agg gat gag att ggg ggc atg act gat ggc atg    1444
Ser Phe Gly Leu Lys Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met
    380                 385                 390                 395

cag ctc ttt gac cgc atc agc acc gcg ggc tac agc atc cca gag ctg    1492
Gln Leu Phe Asp Arg Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu
            400                 405                 410

ctc aca aag ttg gtg cag atc gag cgg ctg gat gct gtg gag tcc ttg    1540
Leu Thr Lys Leu Val Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu
            415                 420                 425

tgt gca gac ata ttg gag tgg gct ggg gtt gta cca cct gcc tcc cca    1588
Cys Ala Asp Ile Leu Glu Trp Ala Gly Val Val Pro Pro Ala Ser Pro
            430                 435                 440

ccc cca gct gcg tcc tga agagttgtct tggactgtct tccctgggac    1636
Pro Pro Ala Ala Ser
    445
```

cagctgggga tccaatgaag tcacgaccga cagctgtgag tgatgctatc agactgccaa 1696

aactcaaggc atttcctggt gggtcactgt attccttagg ctgccctaag tagttcattg 1756

agcactcaaa tgaaccaaac catgtgggaa ggacacaggt gaagaatctg atcctgtctt 1816

ttaaggaggc acttagtgag agatgggagc atggtataga ccgtgttacc aaaacatcac 1876

ctaggcaaat gaagggatgc ttttttaaaa agtagcaaaa gttataaggg tgatagagtc 1936

tcaaggggtt gaaagtggga acatcctaat gaagaaaata acttcaaggt tttagtaaaa 1996

cggttacaaa gtacaggcat cccacatcct tcatggcctc agacagagca tggtttgctg 2056

gcatgcccta tggtttcaga ggtaactcga cctgtgtttg cagtcacaca ccatggtata 2116

agccttgcag tcactagtgg aagaactcac catgtgtcac tgacatacaa ggcgtgtgtc 2176

tgtccagtca caagtgtggg cagatctggc ctccagcacc actcgcagcc acagcagtta 2236

caatgtcagg cttgtcttgc ttcaaaggga cgtgcgtcct atctagagaa ggaaatggtg 2296

acttgctcag agtttgacca tgcctgattc ctgggtgagg ctcgagtgag ttcaggcaca 2356

acatcctgag ccagtgaggg gtggtgcagc ccgagacgca gtacagagct ggggtctgag 2416

gtcctgggca ctgggagagt cattcaaagt gtctgtctcc tccagactta gcttctctta 2476

ggtgagagag gttggtattc acatctgtag tcaggaatgt tgaggctcca gtgagcgaaa 2536

gggtgagtga aagaacacgg aggcagaaga gaagaggcca gaggagcctc catggggtaa 2596

13

```
atacagtgtg ggtggccaca aaaaatgaga gtcaagggaa acgcagccgc cattctcata 2656

taagggcaac tgtaggactg agcgtttaca gggcttataa acagccattg ctcttggcat 2716

attctcttac tgcacctgta actgccagga aatgggagcc aaggaaactt ccccggcagg 2776

gggttaatgc caagctggct gctgggctcc ctcccagagc gctgactgca gagaatgctt 2836

cctttcagta aagctctggt ttagaaggcg gttgggtttt tttgttttac aaggcctatg 2896

actgaacaaa ggctttggag agcaatcagt ggtgtgttta aaaccatcaa gccatttccc 2956

accantgaat atagaccata ctgtgagagg accataatta ggtcctgaat ttttaatatg 3016

atcattttcc tgtgtctgtc tgtgcagtgt tttttttttt tttttaaag aaggcattta 3076

ctccattttg caagttaaat gtctgcttaa ttgtcctttt aattcctgag accctgcagt 3136

gtcccttacc cctggtcttc cataatgacg ctgcgattcc ccttaattag acttgtaaat 3196

gtcatgcgtg atgagtgagc aggtcgagga cagcaggctc ttctccaact gtcattgtgc 3256

tgaagaatgg gcagctgcag ccagcggtgt gggctgccct ccattcacac taataggttt 3316

caaggcctga ggcagccagc atccttgttg tttcctagac tccctgcttg ctgctttagg 3376

ggagccagtt cccttgtcat ttaattaaca tggcaataaa ttctggnagg gttggttggc 3436

ttcagtgtgc tttgccaacc aacaagacca cagtgacttt tggtgaccaa tggtggaact 3496

ccacgctgcc atgtttgttt ggagactgtt attattttt cagtaattaa aggtatttag 3556

taaacaccca agctaggttt gagggcctga gccagtgaag ttttaattgt gaatattta 3616

tataattttg tttatgtaaa ttattatatt tttataagct caataaacat attgatnaaa 3676

agggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa aaaa                   3720
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<210> 13
<211> 1347
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1347)

<400> 13
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atg gcc cac gtc ggg gac tgc aaa tgg atg tcc tgg ctc cca gtg ctg    48
Met Ala His Val Gly Asp Cys Lys Trp Met Ser Trp Leu Pro Val Leu
1               5                   10                  15

gtg gtg tct ctg atg tgc tca gcc aag gcg gag gac tcc aac tgt ggt    96
Val Val Ser Leu Met Cys Ser Ala Lys Ala Glu Asp Ser Asn Cys Gly
```

14

```
gag aac gaa tac cac aac cag act acc ggg ctg tgc cag cag tgt cct    144
Glu Asn Glu Tyr His Asn Gln Thr Thr Gly Leu Cys Gln Gln Cys Pro
            35                  40                  45

cca tgc aga cca ggg gag gag ccc tac atg tcc tgt gga tac ggc act    192
Pro Cys Arg Pro Gly Glu Glu Pro Tyr Met Ser Cys Gly Tyr Gly Thr
        50                  55                  60

aaa gac gac gac tat ggc tgt gtg ccc tgc cct gca gag aag ttc tcc    240
Lys Asp Asp Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu Lys Phe Ser
65                  70                  75                  80

aaa gga ggt tat cag ata tgc agg cgc cac aaa gac tgt gag ggc ttc    288
Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys Glu Gly Phe
                85                  90                  95

ttc cgg gcc act gtg ctg aca cca gga gac atg gaa aac gac gct gag    336
Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn Asp Ala Glu
            100                 105                 110

tgt ggc cca tgt ctc cct ggc tac tac atg ctg gaa aac aga ccc agg    384
Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn Arg Pro Arg
            115                 120                 125

aac atc tat ggc atg gtc tgc tac tcc tgt ctc ttg gca cct ccc aac    432
Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala Pro Pro Asn
        130                 135                 140

acc aag gaa tgt gtg gga gcc act tct ggg gtt tca gca cac tca tcc    480
Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Val Ser Ala His Ser Ser
145                 150                 155                 160

agc act tcc ggt ggc agc acc ttg tct ccc ttc cag cat gct cac aaa    528
Ser Thr Ser Gly Gly Ser Thr Leu Ser Pro Phe Gln His Ala His Lys
                165                 170                 175

gag ctc tca ggc caa gga cac ctg gcc acc gcc ctg att att gcc atg    576
Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile Ile Ala Met
            180                 185                 190

tct acg atc ttc atc atg gcc att gcc atc gtc ctc atc atc atg ttc    624
Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile Ile Met Phe
        195                 200                 205

tac atc atg aag act aag ccg tca gct cca gcc tgc tgt agc agt ccc    672
Tyr Ile Met Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys Ser Ser Pro
        210                 215                 220

cca gga aag agc gca gaa gcc cca gct aac aca cac gag gag aaa aaa    720
Pro Gly Lys Ser Ala Glu Ala Pro Ala Asn Thr His Glu Glu Lys Lys
225                 230                 235                 240

gag gcc cca gac agt gtg gtg acg ttc cct gag aat ggt gag ttc cag    768
Glu Ala Pro Asp Ser Val Val Thr Phe Pro Glu Asn Gly Glu Phe Gln
```

15

```
aag ctg aca gca aca ccc aca aag acc ccc aaa agt gag aat gat gcc   816
Lys Leu Thr Ala Thr Pro Thr Lys Thr Pro Lys Ser Glu Asn Asp Ala
        260         265         270

tcc tct gag aac gag cag ttg cta agt cgc agt gtg gac agt gat gaa   864
Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp Ser Asp Glu
        275         280         285

gag cca gcc ccg gac aag cag ggg tcc cca gag cta tgt ctg ctg tcg   912
Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys Leu Leu Ser
        290         295         300

cta gtt cac ctg gcc agg gag aag tct gtg acc agt aac aag tct gct   960
Leu Val His Leu Ala Arg Glu Lys Ser Val Thr Ser Asn Lys Ser Ala
305             310         315             320

ggg atc cag agc cgg agg aaa aag ata ctg gat gtg tat gcc aac gtg   1008
Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr Ala Asn Val
            325         330             335

tgt ggt gtt gtt gaa ggt ctc agc ccc acc gag ttg ccg ttt gac tgc   1056
Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro Phe Asp Cys
            340         345             350

ctt gag aag aca agc cga atg ctc agc tct aca tac aac tct gag aag   1104
Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn Ser Glu Lys
        355         360             365

gcg gtc gtg aaa aca tgg cgc cac ctt gcc gag agc ttt gga ctg aag   1152
Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe Gly Leu Lys
370             375             380

agg gat gag att ggg ggc atg act gat ggc atg cag ctc ttt gac cgc   1200
Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu Phe Asp Arg
385             390         395             400

atc agc acc gcg ggc tac agc atc cca gag ctg ctc aca aag ttg gtg   1248
Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr Lys Leu Val
            405             410             415

cag atc gag cgg ctg gat gct gtg gag tcc ttg tgt gca gac ata ttg   1296
Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala Asp Ile Leu
        420             425             430

gag tgg gct ggg gtt gta cca cct gcc tcc cca ccc cca gct gcg tcc   1344
Glu Trp Ala Gly Val Val Pro Pro Ala Ser Pro Pro Pro Ala Ala Ser
        435             440             445

tga
                                                                  1347
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<210> 14
<211> 1176

16

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1176)

<400> 14
atg	ggc	tac	ccg	gag	gtg	gag	cgc	agg	gaa	ctc	ctg	cct	gca	gca	gcg	48
Met	Gly	Tyr	Pro	Glu	Val	Glu	Arg	Arg	Glu	Leu	Leu	Pro	Ala	Ala	Ala	
1				5					10					15		

ccg	cgg	gag	cga	ggg	agc	cag	ggc	tgc	ggg	tgt	ggc	ggg	gcc	cct	gcc	96
Pro	Arg	Glu	Arg	Gly	Ser	Gln	Gly	Cys	Gly	Cys	Gly	Gly	Ala	Pro	Ala	
		20					25					30				

cgg	gcg	ggc	gaa	ggg	aac	agc	tgc	ctg	ctc	ttc	ctg	ggt	ttc	ttt	ggc	144
Arg	Ala	Gly	Glu	Gly	Asn	Ser	Cys	Leu	Leu	Phe	Leu	Gly	Phe	Phe	Gly	
		35					40					45				

ctc	tcg	ctg	gcc	ctc	cac	ctg	ctg	acg	ttg	tgc	tgc	tac	cta	gag	ttg	192
Leu	Ser	Leu	Ala	Leu	His	Leu	Leu	Thr	Leu	Cys	Cys	Tyr	Leu	Glu	Leu	
		50					55					60				

cgc	tcg	gag	ttg	cgg	cgg	gaa	cgt	gga	gcc	gag	tcc	cgc	ctt	ggc	ggc	240
Arg	Ser	Glu	Leu	Arg	Arg	Glu	Arg	Gly	Ala	Glu	Ser	Arg	Leu	Gly	Gly	
65					70					75					80	

tcg	ggc	acc	cct	ggc	acc	tct	ggc	acc	cta	agc	agc	ctc	ggt	ggc	ctc	288
Ser	Gly	Thr	Pro	Gly	Thr	Ser	Gly	Thr	Leu	Ser	Ser	Leu	Gly	Gly	Leu	
			85					90					95			

gac	cct	gac	agc	ccc	atc	acc	agt	cac	ctt	ggg	cag	ccg	tca	cct	aag	336
Asp	Pro	Asp	Ser	Pro	Ile	Thr	Ser	His	Leu	Gly	Gln	Pro	Ser	Pro	Lys	
			100					105					110			

cag	cag	cca	ttg	gaa	ccg	gga	gaa	gcc	gca	ctc	cac	tct	gac	tcc	cag	384
Gln	Gln	Pro	Leu	Glu	Pro	Gly	Glu	Ala	Ala	Leu	His	Ser	Asp	Ser	Gln	
		115					120					125				

gac	ggg	cac	cag	atg	gcc	cta	ttg	aat	ttc	ttc	ttc	cct	gat	gaa	aag	432
Asp	Gly	His	Gln	Met	Ala	Leu	Leu	Asn	Phe	Phe	Phe	Pro	Asp	Glu	Lys	
	130				135					140						

cca	tac	tct	gaa	gaa	gaa	agt	agg	cgt	gtt	cgc	cgc	aat	aaa	aga	agc	480
Pro	Tyr	Ser	Glu	Glu	Glu	Ser	Arg	Arg	Val	Arg	Arg	Asn	Lys	Arg	Ser	
145					150					155					160	

aaa	agc	aat	gaa	gga	gca	gat	ggc	cca	gtt	aaa	aac	aag	aaa	aag	gga	528
Lys	Ser	Asn	Glu	Gly	Ala	Asp	Gly	Pro	Val	Lys	Asn	Lys	Lys	Lys	Gly	
			165					170					175			

aag	aaa	gca	gga	cct	cct	gga	ccc	aat	ggc	cct	cca	gga	ccc	cca	gga	576
Lys	Lys	Ala	Gly	Pro	Pro	Gly	Pro	Asn	Gly	Pro	Pro	Gly	Pro	Pro	Gly	
		180					185					190				

17

```
cct cca gga ccc cag gga ccc cca gga att cca ggg att cct gga att    624
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
        195                 200                 205

cca gga aca act gtt atg gga cca cct ggt cct cca ggt cct cct ggt    672
Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
        210                 215                 220

cct caa gga ccc cct ggc ctc cag gga cct tct ggt gct gct gat aaa    720
Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225                 230                 235                 240

gct gga act cga gaa aac cag cca gct gtg gtg cat cta cag ggc caa    768
Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
                245                 250                 255

ggg tca gca att caa gtc aag aat gat ctt tca ggt gga gtg ctc aat    816
Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
                260                 265                 270

gac tgg tct cgc atc act atg aac ccc aag gtg ttt aag cta cat ccc    864
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
        275                 280                 285

cgc agc ggg gag ctg gag gta ctg gtg gac ggc acc tac ttc atc tat    912
Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
    290                 295                 300

agt cag gta gaa gta tac tac atc aac ttc act gac ttt gcc agc tat    960
Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
305                 310                 315                 320

gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc aca cgc agc atc   1008
Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
                325                 330                 335

gag acg ggc aag acc aac tac aac act tgc tat acc gca ggc gtc tgc   1056
Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
                340                 345                 350

ctc ctc aag gcc cgg cag aag atc gcc gtc aag atg gtg cac gct gac   1104
Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
        355                 360                 365

atc tcc atc aac atg agc aag cac acc acg ttc ttt ggg gcc atc agg   1152
Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
    370                 375                 380

ctg ggt gaa gcc cct gca tcc tag
Leu Gly Glu Ala Pro Ala Ser                                        1176
385                 390


<210> 15
<211> 1134
<212> DNA
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<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1134)

<400> 15

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atg ggc tac cca gag gta gag cgc agg gaa ccc ctg cct gcg gca gcg       48
Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Pro Leu Pro Ala Ala Ala
1               5                   10                  15

cca agg gag cgg ggc agc cag ggc tgc ggc tgt cgc ggg gcc cct gct       96
Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Arg Gly Ala Pro Ala
            20                  25                  30

cgg gcg ggc gaa ggg aac agc tgc cgg ctc ttc ctg ggt ttc ttt ggc      144
Arg Ala Gly Glu Gly Asn Ser Cys Arg Leu Phe Leu Gly Phe Phe Gly
        35                  40                  45

ctc tcg ctg gcc ctc cac ctg ctg acg ctg tgc tgc tac cta gag ttg      192
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
        50                  55                  60

cgg tcc gaa ttg cgg cgg gaa cgg gga acc gag tcc cgc ctc ggt ggc      240
Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr Glu Ser Arg Leu Gly Gly
65                  70                  75                  80

ccg ggt gct cct ggc acc tct ggc acc cta agc agc cct ggg agc ctc      288
Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu Ser Ser Pro Gly Ser Leu
                85                  90                  95

gac ccg gtg ggt ccc atc acc cgc cac ctg ggg cag ccg tcc ttt caa      336
Asp Pro Val Gly Pro Ile Thr Arg His Leu Gly Gln Pro Ser Phe Gln
            100                 105                 110

cag cag cct ttg gaa ccg gga gaa gat cca ctc ccc cct gag tcc cag      384
Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro Leu Pro Pro Glu Ser Gln
            115                 120                 125

gac cgg cac cag atg gcc ctc ctg aat ttc ttc ttt cct gat gaa aag      432
Asp Arg His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
    130                 135                 140

gca tat tct gaa gag gaa agt agg cgt gtt cgc cgc aat aag aga agc      480
Ala Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145                 150                 155                 160

aaa agt ggt gaa gga gca gat ggt cct gtt aaa aac aag aaa aag gga      528
Lys Ser Gly Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
                165                 170                 175

aag aag gca ggg cca cct ggg ccc aac ggc ccc cca gga cct cca gga      576
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
            180                 185                 190

cct ccg gga ccc cag gga cct cca ggg att cca gga att cct ggg att      624
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
```

19

```
        Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
                195                     200                 205

        cca gga aca act gtt atg gga cca cct ggc cca cct ggc cct cct ggt    672
        Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
                210                     215                 220

        cct caa gga ccc cct ggc ctc caa gga cct tct ggt gct gct gat aaa    720
        Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
        225                     230                 235                 240

        act gga act cgg gaa aat cag cca gct gtg gtg cat ctg cag ggc caa    768
        Thr Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
                            245                 250                 255

        ggg tca gca att caa gtc aaa aat gat ctt tca ggt gga gtg ctc aat    816
        Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
                        260                 265                 270

        gac tgg tct cgc atc act atg aac cct aag gtg ttt aaa cta cat ccc    864
        Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
                    275                 280                 285

        cgc agc ggg gag ctg gag gtc tac tac atc aac ttc act gac ttt gcc    912
        Arg Ser Gly Glu Leu Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala
                290                 295                 300

        agc tac gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc acc cgc    960
        Ser Tyr Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg
        305                     310                 315                 320

        agc att gag aca ggg aag acc aac tac aac act tgc tat act gca ggc   1008
        Ser Ile Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly
                            325                 330                 335

        gtg tgc ctc ctc aag gcc agg cag aaa atc gcc gtg aag atg gtg cac   1056
        Val Cys Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His
                        340                 345                 350

        gct gac atc tct atc aat atg agc aag cac acc acc ttc ttc ggg gcc   1104
        Ala Asp Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala
                    355                 360                 365

        atc agg ctg ggc gaa gcc cct gca tcc tag                           1134
        Ile Arg Leu Gly Glu Ala Pro Ala Ser
                370                     375
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<210> 16
<211> 1347
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1347)

20

<400> 16

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atg gcc cat gtg ggg gac tgc acg cag acg ccc tgg ctc ccc gtc ctg      48
Met Ala His Val Gly Asp Cys Thr Gln Thr Pro Trp Leu Pro Val Leu
1               5                   10                  15

gtg gtg tct ctg atg tgc tca gcc cga gcg gaa tac tca aac tgc ggt      96
Val Val Ser Leu Met Cys Ser Ala Arg Ala Glu Tyr Ser Asn Cys Gly
            20                  25                  30

gag aac gag tac tac aac cag act acg ggg ctg tgc cag gag tgc ccc     144
Glu Asn Glu Tyr Tyr Asn Gln Thr Thr Gly Leu Cys Gln Glu Cys Pro
        35                  40                  45

ccg tgt ggg ccg gga gag gag ccc tac ctg tcc tgt ggc tac ggc acc     192
Pro Cys Gly Pro Gly Glu Glu Pro Tyr Leu Ser Cys Gly Tyr Gly Thr
    50                  55                  60

aaa gac gag gac tac ggc tgc gtc ccc tgc ccg gcg gag aag ttt tcc     240
Lys Asp Glu Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu Lys Phe Ser
65                  70                  75                  80

aaa gga ggc tac cag ata tgc agg cgt cac aaa gac tgt gag ggc ttc     288
Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys Glu Gly Phe
                85                  90                  95

ttc cgg gcc acc gtg ctg aca cca ggg gac atg gag aat gac gct gag     336
Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn Asp Ala Glu
            100                 105                 110

tgt ggc cct tgc ctc cct ggc tac tac atg ctg gag aac aga ccg agg     384
Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn Arg Pro Arg
        115                 120                 125

aac atc tat ggc atg gtc tgc tac tcc tgc ctc ctg gca ccc ccc aac     432
Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala Pro Pro Asn
        130                 135                 140

acc aag gaa tgt gtg gga gcc act tca gga gct tct gcc aac ttc cct     480
Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Ala Ser Ala Asn Phe Pro
145                 150                 155                 160

ggc acc tcg ggc agc agc acc ctg tct ccc ttc cag cac gcc cac aaa     528
Gly Thr Ser Gly Ser Ser Thr Leu Ser Pro Phe Gln His Ala His Lys
                165                 170                 175

gaa ctc tca ggc caa gga cac ctg gcc act gcc ctg atc att gca atg     576
Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile Ile Ala Met
                180                 185                 190

tcc acc atc ttc atc atg gcc atc gcc atc gtc ctc atc atc atg ttc     624
Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile Ile Met Phe
195                 200                 205

tac atc ctg aag aca aag ccc tct gcc cca gcc tgt tgc acc agc cac     672
Tyr Ile Leu Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys Thr Ser His
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21

ccg ggg aag agc gtg gag gcc caa gtg agc aag gac gag gag aag aaa   720
Pro Gly Lys Ser Val Glu Ala Gln Val Ser Lys Asp Glu Glu Lys Lys
225   230   235   240

gag gcc cca gac aac gtg gtg atg ttc tcc gag aag gat gaa ttt gag   768
Glu Ala Pro Asp Asn Val Val Met Phe Ser Glu Lys Asp Glu Phe Glu
                        245   250   255

aag ctg aca gca act cca gca aag ccc acc aag agc gag aac gat gcc   816
Lys Leu Thr Ala Thr Pro Ala Lys Pro Thr Lys Ser Glu Asn Asp Ala
                    260   265   270

tca tcc gag aat gag cag ctg ctg agc cgg agc gtc gac agt gat gag   864
Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp Ser Asp Glu
                275   280   285

gag ccc gcc cct gac aag cag ggc tcc ccg gag ctg tgc ctg ctg tcg   912
Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys Leu Leu Ser
            290   295   300

ctg gtt cac ctg gcc agg gag aag tct gcc acc agc aac aag tca gcc   960
Leu Val His Leu Ala Arg Glu Lys Ser Ala Thr Ser Asn Lys Ser Ala
305   310   315   320

ggg att caa agc cgg agg aaa aag atc ctc gat gtg tat gcc aac gtg   1008
Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr Ala Asn Val
                    325   330   335

tgt gga gtc gtg gaa ggt ctt agc ccc acg gag ctg cca ttt gat tgc   1056
Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro Phe Asp Cys
                340   345   350

ctc gag aag act agc cga atg ctc agc tcc acg tac aac tct gag aag   1104
Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn Ser Glu Lys
            355   360   365

gct gtt gtg aaa acg tgg cgc cac ctc gcc gag agc ttc ggc ctg aag   1152
Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe Gly Leu Lys
370   375   380

agg gat gag att ggg ggc atg aca gac ggc atg caa ctc ttt gac cgc   1200
Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu Phe Asp Arg
385   390   395   400

atc agc acg gca ggc tac agc atc cct gag cta ctc aca aaa ctg gtg   1248
Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr Lys Leu Val
                    405   410   415

cag att gag cgg ctg gat gct gtg gag tcc ttg tgt gca gac ata ctg   1296
Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala Asp Ile Leu
                420   425   430

gag tgg gcg ggg gtt gtg cca cct gcc tcc cag cca cat gct gca tcc   1344
Glu Trp Ala Gly Val Val Pro Pro Ala Ser Gln Pro His Ala Ala Ser

tga

1347

<210> 17
<211> 448
<212> PRT
<213> Homo sapiens

<400> 17
Met Ala His Val Gly Asp Cys Thr Gln Thr Pro Trp Leu Pro Val Leu
1   5   10   15
Val Val Ser Leu Met Cys Ser Ala Arg Ala Glu Tyr Ser Asn Cys Gly
            20   25   30
Glu Asn Glu Tyr Tyr Asn Gln Thr Thr Gly Leu Cys Gln Glu Cys Pro
        35   40   45
Pro Cys Gly Pro Gly Glu Glu Pro Tyr Leu Ser Cys Gly Tyr Gly Thr
    50   55   60
Lys Asp Glu Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu Lys Phe Ser
65   70   75   80
Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys Glu Gly Phe
                85   90   95
Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn Asp Ala Glu
            100   105   110
Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn Arg Pro Arg
        115   120   125
Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala Pro Pro Asn
    130   135   140
Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Ala Ser Ala Asn Phe Pro
145   150   155   160
Gly Thr Ser Gly Ser Ser Thr Leu Ser Pro Phe Gln His Ala His Lys
                165   170   175
Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile Ile Ala Met
            180   185   190
Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile Ile Met Phe
        195   200   205
Tyr Ile Leu Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys Thr Ser His
    210   215   220
Pro Gly Lys Ser Val Glu Ala Gln Val Ser Lys Asp Glu Glu Lys Lys
225   230   235   240
Glu Ala Pro Asp Asn Val Val Met Phe Ser Glu Lys Asp Glu Phe Glu
                245   250   255
Lys Leu Thr Ala Thr Pro Ala Lys Pro Thr Lys Ser Glu Asn Asp Ala
            260   265   270
Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp Ser Asp Glu
        275   280   285
Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys Leu Leu Ser
    290   295   300
Leu Val His Leu Ala Arg Glu Lys Ser Ala Thr Ser Asn Lys Ser Ala
305   310   315   320
Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr Ala Asn Val
                325   330   335
Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro Phe Asp Cys
            340   345   350

23

Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn Ser Glu Lys
        355   360   365
Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe Gly Leu Lys
        370   375   380
Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu Phe Asp Arg
385   390   395   400
Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr Lys Leu Val
                405   410   415
Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala Asp Ile Leu
        420   425   430
Glu Trp Ala Gly Val Val Pro Pro Ala Ser Gln Pro His Ala Ala Ser
        435   440   445

<210> 18
<211> 4235
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (433)..(1779)

<400> 18
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cccgctccag cctctccagt gctgggagag acctctagat ggtgcaggtg agtttgcaat 120

gagggaaagc ccctcggcaa ggactgagtt tccaaacttg cagacagggc agggagcggt 180

caaggaagag ttcccgggaa gccctttaaa cggaaaggaa gcggggctag tgtcagagag 240

gtgtgccagg tcccaggcag ccctgctgac ccctaaggac atagagtacc tgcttctgag 300

agggctgcca cggtggccac ctgtgaagcc tgtcacccag aactggatgg tacctgactt 360

tcttcataga cccatcttct gctgggactg aagctgacct ccaacagaag ccaggtgagc 420

ccttgggaga gg atg gcc cat gtg ggg gac tgc acg cag acg ccc tgg ctc 471
                Met Ala His Val Gly Asp Cys Thr Gln Thr Pro Trp Leu
                 1   5   10

ccc gtc ctg gtg gtg tct ctg atg tgc tca gcc cga gcg gaa tac tca   519
Pro Val Leu Val Val Ser Leu Met Cys Ser Ala Arg Ala Glu Tyr Ser
        15   20   25

aac tgc ggt gag aac gag tac tac aac cag act acg ggg ctg tgc cag   567
Asn Cys Gly Glu Asn Glu Tyr Tyr Asn Gln Thr Thr Gly Leu Cys Gln
30   35   40   45

gag tgc ccc ccg tgt ggg ccg gga gag gag ccc tac ctg tcc tgt ggc   615
Glu Cys Pro Pro Cys Gly Pro Gly Glu Glu Pro Tyr Leu Ser Cys Gly
                50   55   60

tac ggc acc aaa gac gag gac tac ggc tgc gtc ccc tgc ccg gcg gag   663
24

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Tyr Gly Thr Lys Asp Glu Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu
         65                      70                      75

    aag ttt tcc aaa gga ggc tac cag ata tgc agg cgt cac aaa gac tgt   711
    Lys Phe Ser Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys
             80                      85                      90

    gag ggc ttc ttc cgg gcc acc gtg ctg aca cca ggg gac atg gag aat   759
    Glu Gly Phe Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn
         95                     100                     105

    gac gct gag tgt ggc cct tgc ctc cct ggc tac tac atg ctg gag aac   807
    Asp Ala Glu Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn
    110                     115                     120                125

    aga ccg agg aac atc tat ggc atg gtc tgc tac tcc tgc ctc ctg gca   855
    Arg Pro Arg Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala
                 130                     135                     140

    ccc ccc aac acc aag gaa tgt gtg gga gcc act tca gga gct tct gcc   903
    Pro Pro Asn Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Ala Ser Ala
                     145                     150                 155

    aac ttc cct ggc acc tcg ggc agc agc acc ctg tct ccc ttc cag cac   951
    Asn Phe Pro Gly Thr Ser Gly Ser Ser Thr Leu Ser Pro Phe Gln His
             160                     165                     170

    gcc cac aaa gaa ctc tca ggc caa gga cac ctg gcc act gcc ctg atc   999
    Ala His Lys Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile
        175                     180                     185

    att gca atg tcc acc atc ttc atc atg gcc atc gcc atc gtc ctc atc   1047
    Ile Ala Met Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile
    190                     195                     200                 205

    atc atg ttc tac atc ctg aag aca aag ccc tct gcc cca gcc tgt tgc   1095
    Ile Met Phe Tyr Ile Leu Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys
                 210                     215                     220

    acc agc cac ccg ggg aag agc gtg gag gcc caa gtg agc aag gac gag   1143
    Thr Ser His Pro Gly Lys Ser Val Glu Ala Gln Val Ser Lys Asp Glu
                     225                     230                 235

    gag aag aaa gag gcc cca gac aac gtg gtg atg ttc tcc gag aag gat   1191
    Glu Lys Lys Glu Ala Pro Asp Asn Val Val Met Phe Ser Glu Lys Asp
             240                     245                     250

    gaa ttt gag aag ctg aca gca act cca gca aag ccc acc aag agc gag   1239
    Glu Phe Glu Lys Leu Thr Ala Thr Pro Ala Lys Pro Thr Lys Ser Glu
        255                     260                     265

    aac gat gcc tca tcc gag aat gag cag ctg ctg agc cgg agc gtc gac   1287
    Asn Asp Ala Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp
    270                     275                     280                 285

    agt gat gag gag ccc gcc cct gac aag cag ggc tcc ccg gag ctg tgc   1335
                                        25
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Ser Asp Glu Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys
             290                 295                 300

ctg ctg tcg ctg gtt cac ctg gcc agg gag aag tct gcc acc agc aac    1383
Leu Leu Ser Leu Val His Leu Ala Arg Glu Lys Ser Ala Thr Ser Asn
             305                 310                 315

aag tca gcc ggg att caa agc cgg agg aaa aag atc ctc gat gtg tat    1431
Lys Ser Ala Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr
             320                 325                 330

gcc aac gtg tgt gga gtc gtg gaa ggt ctt agc ccc acg gag ctg cca    1479
Ala Asn Val Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro
             335                 340                 345

ttt gat tgc ctc gag aag act agc cga atg ctc agc tcc acg tac aac    1527
Phe Asp Cys Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn
350                 355                 360                 365

tct gag aag gct gtt gtg aaa acg tgg cgc cac ctc gcc gag agc ttc    1575
Ser Glu Lys Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe
             370                 375                 380

ggc ctg aag agg gat gag att ggg ggc atg aca gac ggc atg caa ctc    1623
Gly Leu Lys Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu
             385                 390                 395

ttt gac cgc atc agc acg gca ggc tac agc atc cct gag cta ctc aca    1671
Phe Asp Arg Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr
             400                 405                 410

aaa ctg gtg cag att gag cgg ctg gat gct gtg gag tcc ttg tgt gca    1719
Lys Leu Val Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala
             415                 420                 425

gac ata ctg gag tgg gcg ggg gtt gtg cca cct gcc tcc cag cca cat    1767
Asp Ile Leu Glu Trp Ala Gly Val Val Pro Pro Ala Ser Gln Pro His
430                 435                 440                 445

gct gca tcc tga aaagcatgcc tgtgggctgt cctcccagga caagccaagg        1819
Ala Ala Ser

atccaacgag ggctctggag ctgtgagtgg tgccaaaaga ctgccaagaa tcaaggcttt 1879

tgtgatatgt caccgtatgc cttaggatgt tcaaggagcc agacgaaata aggcctgtct 1939

tccaatttaa ccaaagataa aggactagag ccgggatact ttcagatgct cgcctgtacc 1999

tcaccaggca gagtaaatat ctactcactc atacagccag cccaccagcc caccattaac 2059

tcactgaaca atgagacaat gttgaggact caaatgaatc aaaccccgtg ggaatgacag 2119

aagtgaagaa tctggtccct gtctttaagg agtttgcact ccagtagaag acagaaggaa 2179

cgtatgttta caaaccactt cactggaaga cgtcaaacaa gctgaatgaa ggggcgctta 2239
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26

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gaaaacgtta atagaagttc taagcgggag atgactccct actgggatga tgaaggatgg 2299

catcctagtg aagaagcagc tcaaacattt tgataaaatg gcaacaaaat gcagacaccc 2359

tgctccaggt attatttcag gtttagtaca agtctgttaa taccctatgt ggtttcatta 2419

ggataacttt ttacctatcc ttgaggtcat ccatattctt acaggccttc cagtcaataa 2479

tggaagagct cactctatac aaaaccaata tgcaaggcat gtgtttgtcc aagcaattgg 2539

atgtgtgcag tagccaattt catttactgc attactcttt ggcctgggaa ccctgtggtc 2599

tgcactacat gtgaatggcc ttccacttca gtcttaggca gatttgacct tttaggggca 2659

gcaatgctga aggacacagc aatttaaatt ataatgtgtc aggctgtgtt ttcacttcaa 2719

acatgtatga gtagtcagct gtaattagag aaatgatgac ttcctaagag ttcagccacg 2779

cataattcta gatttcaaga gcatctaaga cttgtggatt agcctcatgg catgagagtt 2839

tcagactcag ccttctgagc cagtcaggga aagtggagtt ctgcagcgca aatgagagcc 2899

tgggcttggt gtcgagggag ctggcttcta gttgtgccac cttgggcctt gtcttttcct 2959

ctctctgcct cagtttctcg tctgccaatg agatgttagt tagtgattct ataattgggg 3019

caggtagggt tcaggtgagc aaaaagaaag tggagctata ggaaatgcca ggcctttgag 3079

gtgctctatg gaagtcaaca cagtgtggtt tgtccattta aatgggaata aaaacagaaa 3139

aactcagact tggcatttc acaataactg caatggtttg acataacatt tataggcaga 3199

aagttaataa actggcattg ttcttggcat attattgtac tatccctgta actgccaaga 3259

gctcaggagc caggctagtg atcacaccag gggttagagt tcactgctga actccctgat 3319

ggcaggtctg tgtttattac tacattaaaa caaagtctct gacttataaa gcgaggtcgt 3379

aaaaattaca agttgcatga ctgaaaaaat gctttagggg gaaaatcagt catatcttta 3439

acaccaacaa gcaatttccc accaacgaat gtagtacata ctgtgagagg atcataatga 3499

ggtcctgaat atttaatatc atcatttact gtgtctgttt gctgctgttt ttcgaaccta 3559

tttggtttac cctgcaagct aaatactcca cggcagagct taattatcct tttaattcct 3619

ctttgaaatc ctgtggtgcc cccttccccc tgccttgtga tgatgatgag tgagtctccc 3679

cttaattaga ctgcaaatgt cacttgtgat gagtgtgcca ttccaggata acagcttgca 3739

ccctcctcag aatgttttca gcgaaagagt ggggtggctg ttctctgctc ctggtgcttt 3799

ggcctcattt cacactatta gaattctggg gctgtaaggc cagccagtgt cagctcatgt 3859

tccattggct ctccacctgc cattttagg gagctattcc ttatatagtt acaaattccc 3919
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27

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ttgtcattta cttatttgga aacatgggat ttactctgac aagctttagc ctatgttatg 3979

ggattcagaa caatgagatc ataataattc tcactgacca aagctgggac tccatcctgc 4039

cattttgtg tggagatatt cataattctg caatacttta aacatttag aaaacacccc 4099

agggtaggtc tgtggccctt agacagtgaa gtcttaattg tcaatattat ttttgtctaa 4159

ttctgtatat atataactta ttatatttta taatctcaat aaacacatta ataaaaaaaa 4219

aaaaaaaaaa aaaaaa
                                                                    4235


<210> 19
<211> 448
<212> PRT
<213> Homo sapiens

<400> 19
Met Ala His Val Gly Asp Cys Thr Gln Thr Pro Trp Leu Pro Val Leu
1               5                   10                  15
Val Val Ser Leu Met Cys Ser Ala Arg Ala Glu Tyr Ser Asn Cys Gly
            20                  25                  30
Glu Asn Glu Tyr Tyr Asn Gln Thr Thr Gly Leu Cys Gln Glu Cys Pro
        35                  40                  45
Pro Cys Gly Pro Gly Glu Glu Pro Tyr Leu Ser Cys Gly Tyr Gly Thr
    50                  55                  60
Lys Asp Glu Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu Lys Phe Ser
65                  70                  75                  80
Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys Glu Gly Phe
                85                  90                  95
Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn Asp Ala Glu
                100                 105                 110
Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn Arg Pro Arg
            115                 120                 125
Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala Pro Pro Asn
        130                 135                 140
Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Ala Ser Ala Asn Phe Pro
145                 150                 155                 160
Gly Thr Ser Gly Ser Ser Thr Leu Ser Pro Phe Gln His Ala His Lys
                165                 170                 175
Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile Ile Ala Met
            180                 185                 190
Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile Ile Met Phe
        195                 200                 205
Tyr Ile Leu Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys Thr Ser His
    210                 215                 220
Pro Gly Lys Ser Val Glu Ala Gln Val Ser Lys Asp Glu Glu Lys Lys
225                 230                 235                 240
Glu Ala Pro Asp Asn Val Val Met Phe Ser Glu Lys Asp Glu Phe Glu
                245                 250                 255
Lys Leu Thr Ala Thr Pro Ala Lys Pro Thr Lys Ser Glu Asn Asp Ala
            260                 265                 270
Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp Ser Asp Glu
        275                 280                 285
Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys Leu Leu Ser
                            28
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```
        290                      295                    300
    Leu Val His Leu Ala Arg Glu Lys Ser Ala Thr Ser Asn Lys Ser Ala
    305                      310                    315                    320
    Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr Ala Asn Val
                    325                      330                    335
    Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro Phe Asp Cys
                340                      345                    350
    Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn Ser Glu Lys
            355                      360                    365
    Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe Gly Leu Lys
        370                      375                    380
    Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu Phe Asp Arg
    385                      390                    395                    400
    Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr Lys Leu Val
                    405                      410                    415
    Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala Asp Ile Leu
                420                      425                    430
    Glu Trp Ala Gly Val Val Pro Pro Ala Ser Gln Pro His Ala Ala Ser
            435                      440                    445
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<210> 20
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
    Oligonucleotide primers used to amplify exon 5 of
    EDA1-II.

<400> 20
agaaagcagg acctcctgg   19

<210> 21
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
    Oligonucleotide primers used to amplify exon 5 of
    EDA1-II.

<400> 21
ctctcaggat cacccactc   19

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnose ED.

<400> 22
tatgttggct atgactgact gagtgg

26

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnose ED.

<400> 23
ccctaccaag aaggtagttc

20

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnose ED.

<400> 24
ctctcaggat cacccactcc tg

22

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnose ED.

<400> 25
tgtcaattca ccacagggag

20

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

30

<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnos ED.

<400> 26
gaatctagga tgcaggggc

19

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnose ED.

<400> 27
tattgcggcg aacacg

16

<210> 28
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnose ED.

<400> 28
tattgcagcg aacacg

16

<210> 29
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnose ED.

<400> 29
tattgcggca aaacacg

17

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

31

<223> Description of Artificial Sequence:
      Oligonucleotide primers used to screen a BAC
      library.

<400> 30
atcatggctg tgcactctag
                                                              20

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers used to screen a BAC
      library.

<400> 31
acctactgca tgtctgtgga
                                                              20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers used to screen a BAC
      library.

<400> 32
cacatgctca gtgttgtcca
                                                              20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers used to screen a BAC
      library.

<400> 33
acacaggctc agtcatgcgg
                                                              20

<210> 34
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
    Oligonucleotide primers used to clone a murine dl
    gene.

<400> 34
gcggtgaccc gggagatctg aattc

25

<210> 35
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
    Oligonucleotide primers used to clone a murine dl
    gene.

<400> 35
gaattcagat c

11

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
    Oligonucleotide primers used to clone a murine dl
    gene.

<400> 36
ctgagcggaa ttcgtgagac c

21

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
    Oligonucleotide primers used to clone a murine dl
    gene.

<400> 37
ggtctcacga attccgctca gtt

23

<210> 38
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

33

<223> Description of Artificial Sequence:
        Oligonucleotide primers used to clone a murine dl
        gene.

<400> 38
agtgagaatg atgcctcc

                                                                    18

<210> 39
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
        Oligonucleotide primers used to clone a murine dl
        gene.

<400> 39
gcctttgttc agtcatagg

                                                                    19

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
        Oligonucleotide primers used to clone a murine dl
        gene.

<400> 40
cctgagagct ctttgtgag

                                                                    19

<210> 41
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
        Oligonucleotide primers used to clone a murine dl
        gene.

<400> 41
cgggatcctc gagggggggg ggggggggh

                                                                    29

<210> 42
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

34

<223> Description of Artificial Sequence:
       Oligonucleotide primers used to clone a murine dl
       gene.

<400> 42
aagcagagct ccacaatc

18

<210> 43
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers used to clone a murine dl
       gene.

<220>
<221> misc_feature
<222> (38)..(39)
<223> n represents a, c, t, or g; v represents a, g, or
       c

<400> 43
ggccgctctg gacaggatat gtttttttt tttttttvn

39

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers used to clone a murine dl
       gene.

<400> 44
ggaacagtca agagcgagtt

20

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers used to clone a murine dl
       gene.

<400> 45
gcggatccag gccgctctgg acaggatatg

30

35

<210> 46
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 46
tggtgtctct gatgtgc

17

<210> 47
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 47
acagtggccc ggaagaag

18

<210> 48
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 48
ctgcggtgag aacgagtac

19

<210> 49
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 49
ggcaaggtgg cgccatgt

18

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 50
ggcaccaaag acgaggacta

20

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 51
tcagcgtcat tctccatgtc

20

<210> 52
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 52
ctagactcga gaattcgcgg ccgcactagt tttttttttt tttttt

46

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 53
tctggtagcc tcctttggaa

20

37

<210> 54
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 54
ctagactcga gaattcg

17

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 55
tagtcctcgt ctttggtgcc

20

<210> 56
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 56
gagaattcgc ggccgcac

18

<210> 57
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 57
agccccgtag tctggttgta

20

<210> 58
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 58
gcgtcgacag tgatgagga

19

<210> 59
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 59
cagtcttttg gcaccactca

20

<210> 60
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 60
acgtgtgtgg agtcgtgga

19

<210> 61
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 61
ctcgttggat ccttggctt

19

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 62
tacatgctgg agaacagacc

20

<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 63
ttccaaagga ggctaccaga

20

<210> 64
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 64
ttggcagaag ctcctgaagt

20

<210> 65
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 65
tgctcgagat gtgatgaagg

20

<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers that were used to clone
       human DL.

<400> 66
aagcagatgg ccacagaact
                                                                    20

<210> 67
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers that were used to clone
       human DL.

<400> 67
ggagaggatg gcccatgtg
                                                                    19

<210> 68
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers that were used to clone
       human DL.

<400> 68
cagaccatgc catagatgtt c
                                                                    21

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers that were used to clone
       human DL.

<400> 69
acttcaggag cttctgccaa
                                                                    20

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<210> 70
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 70
tcgtccttgc tcacttggg                                               19


<210> 71
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 71
ggatgaattt gagaagctga c                                            21


<210> 72
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 72
ctgacttgtt cgtggtggc                                               19


<210> 73
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that were used to clone
      human DL.

<400> 73
tccacgactc cacacacgt                                               19
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```
<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 74
aaataaaggt agccagaccc                                                    20


<210> 75
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 75
gtaaggggct cagaccact                                                     19


<210> 76
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 76
catgtgtttc taaggaggta c                                                  21


<210> 77
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 77
caacaatgcc acaagcagga                                                    20
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<210> 78
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 78
gtccgtatgg tttggctgc

19

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 79
gccagggttt gccaggag

18

<210> 80
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 80
gtccagctca cctgtctct

19

<210> 81
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 81
accggctctt tcctacacc

19

<210> 82
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers that can be used for
       mutation screening of human DL.

<400> 82
tggagcttct ctggatcatt t

                                                                          21

<210> 83
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers that can be used for
       mutation screening of human DL.

<400> 83
aactccaggt gatcgatacc

                                                                          20

<210> 84
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers that can be used for
       mutation screening of human DL.

<400> 84
ctgggtcatt catgccttct

                                                                          20

<210> 85
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
       Oligonucleotide primers that can be used for
       mutation screening of human DL.

<400> 85
atggtgtgtg gaagccctg

                                                                          19

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<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide primers that can be used for
     mutation screening of human DL.

<400> 86
catgagccaa ttctaactcc t                                               21


<210> 87
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide primers that can be used for
     mutation screening of human DL.

<400> 87
caggaccca gttcagctt                                                   19


<210> 88
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide primers that can be used for
     mutation screening of human DL.

<400> 88
cccaggcact gctaatgac                                                  19


<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide primers that can be used for
     mutation screening of human DL.

<400> 89
ccacatctca cagctcatca                                                 20
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46

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<210> 90
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 90
tttctactgt tgccccttc t                                              21


<210> 91
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 91
cccagccctt catgtcagt                                                19


<210> 92
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 92
tctattgact gtgacttgca                                               20


<210> 93
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used for
      mutation screening of human DL.

<400> 93
ctcgttggat ccttggctt                                                19
```

47

<210> 94
<211> 425
<212> DNA
<213> Homo sapiens

<400> 94
tttttttttt tgggggcaga cggccgaaga gccaggtgtg ccaaggtcat atggcagcag 60
ggctgaacgt gcccgctcca gcctctccag tgctggaaga gacctctaga tggagcaggt 120
gagtttgcaa ttagggaaag cccctcggca aggactgagt ttccaaactt gcagacaggg 180
cagggagcgg tcaaggaaga gttcccggga agccctttaa acggaaagga agcggggcta 240
gtgtcagaga ggtgtgacag gtcccagtca gccctgctgg cccctaagga catagagtac 300
ctgcttctga gagggctgcc acggtggcca cctgtgaagc ctgtcaccca gaactggatg 360
gtacctgact ttcttcatag acccatcttc tgctgggact gaagctgacc tccaacagaa 420
gccag   425

<210> 95
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(434)
<223> n represents a, c, t, or g

<400> 95
gtaagccctg gtcctttcct ctggttttct aaactcttca gctgtggccg agacggaggt 60
gtcatgggct gggagagagg ctgggtgcat ttttgaaatg catgtcattt ttgggttgcg 120
tttgaaggtt tcnccaaacc ctctgagcac gagaaacaca atcactancc tcggtttttaa 180
ccttgggccc tccgtgtgct cctagcctcc tntcaggctc cctcccaggc atggctgcna 240
ggctgggaag gccccagagt cagcccaagt ggcatgggtn cagcttcagc ttcatgtctg 300
cttttctttt aggatgtata gtttcccctc tgtttgctgg aaggcacctt atatccagtg 360
gggttaaata aaggtagcca gaccccccggc tggggtgcta ccgccagtgc ccagctaatg 420
acgcatnnnt tcag   434

<210> 96
<211> 70
<212> DNA
<213> Homo sapiens

<400> 96
gtgagcccct tgggagagga tggcccatgt ggggggactgc acgcagacgc cctggctccc 60
cgtcctggtg   70

<210> 97
<211> 722
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(722)
<223> n is a, c, t or g

48

<400> 97

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gtaagtggtc tgagcccctt accccacag caccctcatc ctcatgatgg ttggactgtt 60
tcttggcctc ttcagctgta aaatgggaat gctgatcata gtccctcctc cacagggttc 120
ttctgagggt gaaatgaaac caggcctgca aagcacagaa ctctgcccca ggctgaagtt 180
acattgattt cgttggtagc tcccttcata gggtctcatg gatataaacg ttcttgattg 240
cttgtttgtg gtgtgataca cacagccctg tgtctatgtg atgagctcat gcttgggggc 300
cgcgcagcta agaaagactt ggaagactca gacccctacc cccatcctcc tggacacgcc 360
ggtgttctga ggagccactg tattagaggc tcagtggggg acagggcgc ctcctccatg 420
accttggcaa gtgcgttgat gaggagaact canagcaggc cttgatggtg ggatggggct 480
tggccagcag gggtgaaggc agggtggttc tagtgggggc tggccgtgcc cangtggatc 540
aaccaggagc cactggagac ttaacagcag tgagcactna caagcggcac cttcccagac 600
cgagccccca gcagagcccc caccgcaggg cacccccttc ctatgtcaac cttggggtct 660
tgcaggagtc acatgtgttt ctaaggaggt acggaggcca caacacccc ctttgttggc 720
ag                                                                722
```

<210> 98
<211> 123
<212> DNA
<213> Homo sapiens

<400> 98

```
gtgtctctga tgtgctcagc ccgagcggaa tactcaaact gcggtgagaa cgagtactac 60
aaccagacta cggggctgtg ccaggagtgc cccccgtgtg ggccgggaga ggagccctac 120
ctg                                                                123
```

<210> 99
<211> 740
<212> DNA
<213> Homo sapiens

<400> 99

```
gtaaggaccc agccctcctg gagcctggtg cgctctcagg ggaggcctcc tgcttgtggc 60
attgttgccc tgagcctgcc ttgctgtgtg aggggatgcc aggtatatc aaaccagccg 120
gtcacgctcc ctggacgttg agattgatgg caagagctgc cgtgagccca ggaatggcac 180
tcaccagcta agcattcata aacagatttt tcaggagttc tgaaatgttt ttaaaggatc 240
actttcccac tctaccctga ttaaatgagc gtcagatcat ctgattggaa gcaggattga 300
aatattctcc agtactagta catttttttcc tgagtgctgc atctccctcc gcctctgggc 360
aagctaagc tgagtgttct gttcagcact aagggaaacc tccggggttt cagtgtccgg 420
ttcttgtagc aagctgagga aagtcagatg ccaagtgcta cctgcactgc ctgggcattc 480
cagcagctcg ctgaattcat ctcggggagg ctcagaaaag gggcagcatc tggagcctga 540
gagtggcgag gagaggggca agcccagagc atgagctggt tcctgggggg ttttgcagtt 600
aggacaactc aggaaaccaa ggcccggcaa gagtagcttc tggagacagc tggcacgtca 660
ctgcccaagg actgtgggcc gagtccgtat ggtttggctg ctgcactcac ctgtgtcccc 720
tgtcctcttt ccctggacag                                              740
```

<210> 100
<211> 182
<212> DNA
<213> Homo sapiens

<400> 100

```
tcctgtggct acggcaccaa agacgaggac tacggctgcg tcccctgccc ggcggagaag 60
```

```
ttttccaaag gaggctacca gatatgcagg cgtcacaaag actgtgaggg cttcttccgg 120
gccaccgtgc tgacaccagg ggacatggag aatgacgctg agtgtggccc ttgcctccct 180
gg
                                                                  182


<210> 101
<211> 1169
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1169)
<223> n represents a, c, t, or g

<400> 101
gtaagcacag gccctcctgg caaaccctgg catgctttct gcagaaaacc ccgaggggct 60
acgggcaagg accttgggaa caggggtcat ggatactgca ggcctcggtg cagccgcaca 120
cctggccttg gtcccatccc acaaggagca gcatccagga cggagagtcc tggcccctcc 180
ggtggacagg cagcccatca ggctctgcct ctgtgtctcc taagtggcca ttaaccatca 240
taatatcttc tgaccaccaa aaggaaacaa attgcttgaa tacttacagt gcagtagccc 300
atgtgaaaca ctttgggaaa aagaaaactn naatttnatg caaaaagcag tattttnagt 360
attctggnaa cactctggnn aanctactaa taanntanat ntgagaaaag aaatatnant 420
gangagatta tgannncgaa gnnaagnnan gnanaancan annaggntnn agaaaatgag 480
gttgnnaang antnataana tagnacanng ntgatatnca tnggaaagta aacngcntga 540
gnannagtga tttgtgatng ccagggtatt cntngaggga aaacangact attggancag 600
anngtgngga aaggnacaaa cgntgtntna ncataganaa nntagagttg ntgggtgggc 660
attnnaanna gcnggtaaag aatagcttgn aagtngncaa ggggtnccag aggcaannnt 720
aatgcctata natcccataa gnntgcaggc tantggngan ggtgctnaca aagagcatgt 780
tcctcctcca ggaaggtctg gccttngttg gtgtnacccc tgggggggcta ancaggccnt 840
acatgtgggg gcacagggat atttctggtg natgatgtga tggcacacac actaaacaca 900
gccaccagag agaggaacca gaaaggggct gagatcaaaa gaaaggccca cgttggcagc 960
tcaatattgt taaaagaatg ctccatttca agacaggctg aaaccccaag gaaactgagt 1020
ggacagagca ggtgactgag tgggcgtggc ctcatgcccg acttgattgt gggcctgcag 1080
actggccacc gtgctctctg caccagtccc tgcctgtgtg ctgtccagct cacctgtcta 1140
ctgttttgtc cttgtgctct ccnccgtag 1169
                                                                 1169


<210> 102
<211> 86
<212> DNA
<213> Homo sapiens

<400> 102
ctactacatg ctggagaaca gaccgaggaa catctatggc atggtctgct actcctgcct 60
cctggcaccc cccaacacca aggaat
                                                                   86


<210> 103
<211> 484
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(484)
```

50

<223> n represents a, c, t, or g

<400> 103
gtgagtgtct ttgtccttcc accagcacgg tatttgttca ggcacggatc tctttcacta 60
cagagggtgt aggaaagagc cggtcctggc acctggacaa ggtgaatcac agtaacagca 120
ctagtgaaag tgctcctgtg gcctgtccag gcaggtctat gaagggaggg gcgtttgcca 180
catctgagcc ttgagtcaga ggctgaggtt ctagtgcagg ttggccacca gctacctgac 240
aagtcactta acctccatga gcctcggttt tctcatcggt aatatggggg tgaagaaagn 300
acaatancga tgactcttta gggttcatta aacagtctaa gaaatacaaa tatttagctc 360
ccctcagcca tcactgcctc aggcccattc atgatcatga atccagatcc atgagctctg 420
tggcagcgtg ctttgaaggt ggagcttctc tggatcattt gagggactct attttgcctt 480
gcag
                                                                  484

<210> 104
<211> 87
<212> DNA
<213> Homo sapiens

<400> 104
gtgtgggagc cacttcagga gcttctgcca acttccctgg cacctcgggc agcagcaccc 60
tgtctccctt ccagcacgcc cacaaag
                              87

<210> 105
<211> 799
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(799)
<223> n represents a, c, t, or g

<400> 105
gtgaggaggg tgctcaggta tcgatcacct ggagttaggt ggtactcgga tgaaagctca 60
gaagaggaga ggaaatgatc atgagtgatg attatggtgc gcttccccac ctggcctcac 120
ctccctaatg taattgaatg acatgttgcc ccccgtgcag gaagtcatta tatctgcaat 180
cagagttgat ccctctatgg gtgtcctggg accgctggga ggtgctggtg gtgaaggcgg 240
gggcatagcg gcaggtggac agcacaggca gctgcaagcc cggccaggag gagagaccag 300
gcgtcctggg ctttggtttg gccgngagtt aacagcaatt ctatcactgg ttttcatata 360
aacatgctga ccatagcact ttaatattaa cttgcanaan gtncattttc attctncctt 420
aaccagggaa gangggatcg nggaggaccc caangtttan tntgcctctc acanttagnc 480
ccccacntgg cttgncntna aggttgccaa agcagtagna gcgagaagca agctcccttа 540
ggaacaatna ggtanccсса gaaaaagtct gganaggcca agtctgaggg cagcgagcag 600
gggttgtggg cagtcctggt ctggcagcca aaaccagcgc gnaggatttg gttctcagtc 660
taagcaagca cctcagattt cagggttccc tgaaagcatc ccaggggcag ggccattgct 720
tccaggggcc ggagtcctgg agggaagacc agcagggatc ctgagctctg ggtcattcat 780
gccttctctc cacccacag
                      799

<210> 106
<211> 126
<212> DNA
<213> Homo sapiens

51

<400> 106
aactctcagg ccaaggacac ctggccactg ccctgatcat tgcaatgtcc accatcttca 60
tcatggccat cgccatcgtc ctcatcatca tgttctacat cctgaagaca aagccctctg 120
ccccag   126

<210> 107
<211> 96
<212> DNA
<213> Homo sapiens

<400> 107
gtgacggccc ccatgcgccg gtgccctgcc tcctggactc tccgtcaact ccccctgtcg 60
gagagcctgg ctgctcactc cctcctctct ccccag   96

<210> 108
<211> 75
<212> DNA
<213> Homo sapiens

<400> 108
cctgttgcac cagccacccg gggaagagcg tggaggccca agtgagcaag gacgaggaga 60
agaaagaggc cccag   75

<210> 109
<211> 243
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(243)
<223> n represents a, c, t, or g

<400> 109
gtctgtgaac cagggcttcc acacaccatg tgcacggtgc ccatctctgg gtggagggcg 60
ttcccagaag cagcctcctc gctgcttctg ctctcacatg ctgaaccata ctgtgcttac 120
cgtggggtgg tgccacacag acaccgggca gctctgccca acaggaagag cagggttggg 180
ctgagcgcan agccatgagc caattctaac tcctatctcc ccaacctccc catttccctg 240
cag   243

<210> 110
<211> 73
<212> DNA
<213> Homo sapiens

<400> 110
acaacgtggt gatgttctcc gagaaggatg aatttgagaa gctgacagca acttcagcaa 60
agcccaccaa gag   73

<210> 111
<211> 1174

52

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1174)
<223> n represents a, c, t, or g

<400> 111
gtatgtggaa gcccccacac caagctgaac tggggtcctg tggatcctga gcagggaggg 60
gttnccaggg tgcagccgag tgaactgaca ggctagcctg ggacactatg gggacgttcg 120
gcgacagaca gtccccacca cctctttgct gactggcagg ggtcaggtgg tgtgaggagc 180
ctgtggaaac agctgcctgc tgctctcggg tcaggcccct gtccctgcat cctgccaaat 240
tccctgggcc ttcctcctta acatccgaat tcctcatgcc ccttctccag actgggaggg 300
cagaacataa agccaaggat gcatgcctgt tgcggccaac acaccagtac cacccgtgcc 360
ggtgccagta ctgctgccac cgtaatgctg gtaacaaccg tggtgatgac ggctaacagc 420
atttggtgcc tactgcccac caagtgctgg gctagggctg tgaacacatc ctncctccca 480
ccagcccang agcaaggtgc ttggaatcat ccctggttat aggaatacca cactgaggta 540
tggaagttgt cactcgccca aagtcacaca ctagtgaaca canggcttgg ggtccgaagt 600
ccangctccc aangagccac atggngntaa anaggtnagn cagggtcacc cccctaagtt 660
ccaagagggg ggcttttcna ggcacaaagg gttccattna ggttcccttt tcaatgnctt 720
ccagagagcc agcatggatt tcagcgccag cngcatccaa tctgtttgct ttaacatgaa 780
gacaccagtt gaacttgggt gcttactggg attaaataca gagatctagg acatattcaa 840
tgaaccttca cggagcatcc attgtgtgtc aggtagcagg gaaggagagg cccgtggatg 900
cctcccaccc gcagtggcag ccccagcccc ttagacgcct gcaggtcacc caccacggac 960
ttgtttgttt ggaaagaagc aggaagccac cggtgtatgt ctcgtctcat gtccctggt 1020
cccgtgccca caaggtgccc agtaaacacc tgaaaaacaa gtcattgccc cccactgtcc 1080
acagctgggc aatggacaag ttcaccacag gagaacttgt cagggctgca gcccccccag 1140
gcactgctaa tgaccatcgc tcttgttttt gcag 1174

<210> 112
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(160)
<223> n represents a, c, t, or g

<400> 112
cgagaacgat gcctcatcng agaatgagca gctgctgagc cggagcgtcg acagtgatga 60
ggagcccgcc cctgacaagc agggctcccc ggagctgtgc ctgctgtcgc tggttcacct 120
ggccagggag aagtctgcca ccagcaacaa gtcagccggg 160

<210> 113
<211> 226
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(226)
<223> n represents a, c, t, or g

53

<400> 113

```
gtgaggctcc tgcaggtgcc atgatgagct gtgagatgtg gctccctcac agccgcaagg 60
actaaaactt tcttattgaa tcagctctcc tgcaagacgg ggtgtttctc ccagaagtcc 120
aagataggag acctggacag tgacaagttc acagcaagat agtcaaaagg gaaaaaaacc 180
ctttcgtttt tgagttttgt ttttttttn ggngatgana gnctng           226
```

<210> 114
<211> 61
<212> DNA
<213> Homo sapiens

<400> 114

```
attcaaagcc ggaggaaaaa gatcctcgat gtgtatgcca acgtgtgtgg agtcgtggaa 60
g                                                            61
```

<210> 115
<211> 309
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(309)
<223> n represents a, c, t, or g

<400> 115

```
agagtggnng aagagngaag ggaggngaaa aggggngag ngagggaagg aggngggaan 60
nnggagtgag gggggaagg ggnagagngg gnggnagngn gnggngagng gganagngaa 120
agnagtgaga ngggaaggna nagngagnag gggnnangag aaagngggag ngtaggnggc 180
gatgngnnng gtngaaatat tnanagaaat tttttcaaat aattttatt tcatttaaat 240
aattttcag tgttgacctt ctattgactg tgacttgcaa catctaactg tggccattgg 300
tgtctgtag                                                    309
```

<210> 116
<211> 2781
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(2781)
<223> n represents a, c, t, or g

<400> 116

```
gtcttagccc cacggagctg ccatttgatt gcctcgagaa gactagccga atgctcagct 60
ccacgtacaa ctctgagaag gctgttgtga aaacgtggcg ccacctcgcc gagagcttcg 120
gcctgaagag ggatgagatt gggggcatga cagacggcat gcaactcttt gaccgcatca 180
gcacggcagg ctacagcatc cctgagctac tcacaaaact ggtgcagatt gagcggctgg 240
atgctgtgga gtccttgtgt gcagacatac tggagtgggc gggggttgtg ccacctgcct 300
cccagccaca tgctgcatcc tgaaaagcat gcctgtgggc tgtcctccca ggacaagcca 360
aggatccaac gagggctctg gagctgtgag tggtgccaaa agactgccaa gaatcaaggc 420
ttttgtgata tgtcaccgta tgccttagga tgttcaagga gccagacgaa ataaggcctg 480
```

```
tcttccaatt taaccaaaga taaaggacta gagccgggat actttcanat gctcgcctgt 540
acctcaccag gcagagtaaa tatctactca ctcatacagc cagcccacca gcccaccatt 600
aactcactga acaatgagac aatgtngagg actcaaatga atcaaacccc gtgggaatga 660
cagantgaag aatctggtcc ctgtctttaa ggagtttgca ctccagtaga agacagaagg 720
aacgtatgtt tacaaaccac ttcactggaa gacgtcaaac aagctgaatg aaggggcgct 780
tagaaaacgt taatagaagt tctaagcggg agatgactcc ctactgggat gatgaaggat 840
ggcatcctag tgaagaagca gctcaaacat tttgataaaa tggcaacaaa atgcagacac 900
cctgctccag gtattatttc aggtttagta caagtctgtt aataccctat gtggtttcat 960
taggataact ttttacctat ccttgaggtc atccatattc ttacaggcct tccagtcaat 1020
aatggaagag ctcactctat acaaaaccaa tatgcaaggc atgtgtttgt ccaagcaatt 1080
ggatgtgtgc agtagccaat ttcatttact gcattactct ttggcctggg aaccctgtgg 1140
tctgcactac atgtgaatgg ccttccactt caagtcttag gcagatttga ccttttaggg 1200
gcagcaatgc tgaaggacac agcaatttaa attataatgt gtcaggctgt gttttcactt 1260
caaacatgta tgagtagtca gctgtaatta gagaaatgat gacttcctaa gagttcagcc 1320
acgcataatt ctagatttca agagcatcta agacttgtgg attagcctca tggcatgaga 1380
gtttcagact cagccttctg agccagtcag ggaaagtgga gttctgcagc gcaaatgaga 1440
gcctgggctt ggtgtcgagg gagctggctt ctagttgtgc caccttgggc cttgtctttt 1500
cctctctctg cctcagtttc tcgtctgcca atgagatgtt agttagtgat tctataattg 1560
gggcaggtag ggttcaggtg agcaaaaaga aagtggagct ataggaaatg ccaggccttt 1620
gaggtgctct atggaagtca acacagtgtg gtttgtccat ttaaatggga ataaaaacag 1680
aaaaactcag acttggcatt ttcacaataa ctgcaatggt ttgacataac atttataggc 1740
agaaagttaa taaactggca ttgttcttgg catattattg tactatccct gtaactgcca 1800
agagctcagg agccaggcta gtgatcacac caggggttag agttcactgc tgaactccct 1860
gatggcaggt ctgtgtttat tactacatta aaacaaagtc tctgacttat aaagcgaggt 1920
cgtaaaaatt acaagttgca tgactgaaaa aatgctttag ggggaaaatc agtcatatct 1980
ttaacaccaa caagcaattt cccaccaacg aatgtagtac atactgtgag aggatcataa 2040
tgaggtcctg aatatttaat atcatcattt actgtgtctg tttgctgctg tttttcgaac 2100
ctatttggtt taccctgcaa gctaaatact ccacggcaga ncttaattat ccttttaatt 2160
cctctttgaa atcctgtggt gccccccttcc ccctgccttg tgatgatgat gagtgagtct 2220
ccccttaatt agactgcaaa tgtcacttgt gatgagtgtg ccattccagg ataacagctt 2280
gcaccctcct cagaatgttt tcagcgaaag agtgggggtgg ctgttctctg ctcctggtgc 2340
tttggcctca tttcacacta ttagaattct ggggctgtaa ggccagccag tgtcagctca 2400
tgttccattg gctctccacc tgccattttt agggagctat tccttatata gttacaaatt 2460
cccttgtcat ttacttattt ggaaacatgg gatttactct gacaagcttt agcctatgtt 2520
atgggattca gaacaatgag atcataataa ttctcactga ccaaagctgg gactccatcc 2580
tgccattttt gtgtggagat attcataatt ctgcaatact ttaaaacatt tagaaaacac 2640
cccagggtag gtctgtggcc cttanacagt gaaagtctta attggcaata ttattttttgc 2700
taattctgga tatatataac nnattatatt tataaatctc aataaacccc atttantaaa 2760
aaaaaaaaaa aaaaaaaaaa a                                           2781
```

<210> 117
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers that can be used to
      diagnosis ED.

<400> 117
aaaaagtaac actgatccta ttt   23

<210> 118

55

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used to
diagnosis ED.

<400> 118
agaaagcagg acctcctgg   19

<210> 119
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primer that can be used to amplify
TNF homology domain of mouse dl.

<400> 119
ggattccagg aacaactgtt atgg   24

<210> 120
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primer that can be used to amplify
TNF homology domain of mouse dl.

<400> 120
cctacacaca gcaagcacct tagag   25

<210> 121
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primer that can be used to amplify
TNF homology domain of mouse dl.

<400> 121
gtcgacgaaa atcagccagc tg   22

<210> 122

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primer that can be used to amplify
      TNF homology domain of mouse dl.

<400> 122
aagcttctag gatgcagggg c   21

<210> 123
<211> 17
<212> PRT
<213> Homo sapiens

<400> 123
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 1   5   10   15

Phe

<210> 124
<211> 17
<212> PRT
<213> Homo sapiens

<400> 124
Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln Val Val
 1   5   10   15

Phe

<210> 125
<211> 17
<212> PRT
<213> Homo sapiens

<400> 125
Leu Ala Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly
 1   5   10   15

Tyr

<210> 126
<211> 17
<212> PRT
<213> Homo sapiens

57

<400> 126
Leu Val Ile Asn Glu Ala Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr
1   5   10   15

Phe

<210> 127
<211> 17
<212> PRT
<213> Homo sapiens

<400> 127
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
1   5   10   15

Phe